39. (New) The purified polynucleotide according to Claim 38, wherein said purified polynucleotide further comprises a polynucleotide fragment that is at least 90% homologous to at least 700 consecutive nucleotides of SEQ ID NO: 2.

40. (New) A method of making a polypeptide comprising expressing the sequence corresponding to the open reading frame of a polynucleotide according to Claim 38.

41. (New) A diagnostic reagent for the differential detection of a human endogenous retroviral sequence comprising a polynucleotide having a sequence is selected from the group consisting of SEQ ID NO: 1-22, 28, 37-57, 59-61 and 121-122, a sequence complementary to one of SEQ ID NO: 1-22, 28, 37-57, 59-61 and 121-122, and a sequence that is the reverse complement to one of SEQ ID NO: 1-22, 28, 37-57, 59-61 and 121-122.

42. (New) The diagnostic reagent according to Claim 41, wherein said polynucleotide further comprises a label for detection.

43. (New) The diagnostic reagent according to Claim 41, wherein said polynucleotide is selected from the group consisting of nucleotides 3065-4390 of SEQ ID NO: 3, nucleotides 6965-9550 of SEQ ID NO: 3, and nucleotides 2502-2865 of SEQ ID NO: 3.

44. (New) The diagnostic reagent according to Claim 41, wherein said polynucleotide is selected from the group consisting of SEQ ID NO: 37-57, 59-60 and 121-122 and in that it is capable of being used as a primer.

45. (New) The reagent as claimed in claim 41, wherein said polynucleotide is selected from the group consisting of a fragment of 1505 nucleotides amplified by the pair of primers SEQ ID NO: 37 and SEQ ID NO: 38, a fragment of 2529 nucleotides amplified by the pair of primers SEQ ID NO: 45 and SEQ ID NO: 46, and a fragment of 182 nucleotides, repeated twice, at positions 2502-2611/2613-2865 of SEQ ID NO: 3.

46. (New) A method for the rapid and differential detection of the human endogenous retroviral sequence of the *env* or env and *gag* type, comprising:

(a) contacting a biological sample with at least one diagnostic reagent according to Claim 41, and

(b) detecting a product resulting from a nucleotide sequence-diagnostic reagent interaction.

47. (New) A method for the rapid and differential detection of the human endogenous retroviral sequence of the *env* or env and *gag* type, comprising:

(a) preparing a biological tissue or fluid,

(b) extracting a nucleic acid to be detected,

(c) contacting the nucleic acid with at least one diagnostic reagent according to Claim 41,

(d) conducting at least one gene amplification cycle with the aid of said at least one diagnostic reagent,

(e) detecting a product resulting from a nucleotide sequence-diagnostic reagent interaction, and

(f) comparing the nucleic sequences obtained from said detecting with a polynucleotide comprising a sequence containing a polynucleotide fragment that is at least 80% homologous to at least 190 consecutive nucleotides of SEQ ID NO: 1, wherein said sequence is selected from the group consisting of SEQ ID NOs: 3-5, 7-9, 11-12, 14-16, 18, 20-22, and 61, a sequence complementary to one of SEQ ID NOs: 3-5, 7-9, 11-12, 14-16, 18, 20-22, and 61, and a sequence that is the reverse complement to one of SEQ ID NOs: 3-5, 7-9, 11-12, 14-16, 18, 20-22, and 61.

48. (New) The method according to Claim 47, wherein said comparing is by a technique selected from the group consisting of sequencing, Southern blotting, restriction cleavage, and SSCP.

49. (New) A method of detecting a polypeptide encoded by a polynucleotide comprising a sequence containing a polynucleotide fragment that is at least 80% homologous to at least 190 consecutive nucleotides of SEQ ID NO: 1, wherein said sequence is selected from the group consisting of SEQ ID NOs: 3-5, 7-9, 11-12, 14-16, 18, 20-22, and 61, a sequence complementary to one of SEQ ID NOs: 3-5, 7-9, 11-12, 14-16, 18, 20-22, and 61, and a sequence that is the reverse complement to one of SEQ ID NOs: 3-5, 7-9, 11-12, 14-16, 18, 20-22, and 61, comprising:

collecting messenger RNAs obtained from a control biological sample and from a sample collected from patient, and

analyzing qualitatively and/or quantitatively said mRNAs using the diagnostic aid according to Claim 41 by a technique selected from the group consisting of *in situ* hybridization, by dot-blot, Northern blotting, RNAse mapping and RT-PCR.

50. (New) A recombinant cloning or expression vector comprising the polynucleotide according to Claim 38.

51. (New) A method of making a diagnostic reagent comprising mixing the polynucleotide according to Claim 38 with a suitable medium.

52. (New) A method for the rapid and differential detection of the human endogenous retroviral sequence of the *env* or env and *gag* type, comprising:

(a) making a diagnostic reagent comprising mixing the polynucleotide according to Claim 38 with a suitable medium,

(b) contacting a biological sample with said diagnostic reagent, and

(c) detecting a product resulting from a nucleotide sequence-diagnostic reagent interaction.

53. (New) A method for the rapid and differential detection of the human endogenous retroviral sequence of the *env* or env and *gag* type, comprising:

(a) making a diagnostic reagent comprising mixing the polynucleotide according to Claim 38 with a suitable medium,

(b) preparing a biological tissue or fluid,

(c) extracting a nucleic acid to be detected,

(d) contacting the nucleic acid with said diagnostic reagent,

(e) conducting at least one gene amplification cycle with the aid of said at least one diagnostic reagent,

(f) detecting a product resulting from a nucleotide sequence-diagnostic reagent interaction, and

(g) comparing the nucleic sequences obtained from said detecting with a polynucleotide comprising a sequence containing a polynucleotide fragment that is at least 80% homologous to at least 190 consecutive nucleotides of SEQ ID NO: 1, wherein said sequence is selected from the group consisting of SEQ ID NOs: 3-5, 7-9, 11-12, 14-16, 18, 20-22, and 61, a sequence complementary to one of SEQ ID NOs: 3-5, 7-9, 11-12, 14-16, 18, 20-22, and 61, and a sequence that is the reverse complement to one of SEQ ID NOs: 3-5, 7-9, 11-12, 14-16, 18, 20-22, and 61.

54. (New) The method according to Claim 53, wherein said comparing is by a technique selected from the group consisting of sequencing, Southern blotting, restriction cleavage, and SSCP.

55. (New) A method of making a detection kit, comprising mixing one or more polynucleotides according to Claim 38 with at least one reagent selected from the group consisting of the transcripts and cDNAs of the genomic sequences, which encode all or part of a factor, whose function, regulation/de regulation or alteration is associated with the normal or pathological expression or with the regulation/deregulation of motifs belonging to said HERV-7q family, these sequences corresponding to nucleotide sequences encoding

genes situated in flanking regions situated upstream and/or downstream of a retroviral sequence of said HERV-7q family, of which one of the ends cannot be at a distance exceeding 120 kb.

D concld. 56. (New) The method according to Claim 55, further comprising attaching said polynucleotide and said reagents to a support.

BASIS FOR THE AMENDMENT

Claims 1-37 have been canceled.

Claims 38-56 have been added.

New Claims 38-56 are supported by the claims as originally filed and the specification at pages 1-57, with particular note given to page 5, page 10, and Table II (pages 40-41).

No new matter is believed to have been added by the present amendment.

REMARKS

Claims 38-56 are active in the present application.

Applicants wish to thank Examiner Brown and Examiner Park for the courteous and helpful discussion with their undersigned Representative on June 7, 2002.

Applicants also would like to thank the Examiners for allowing them to elect on additional species contained in SEQ ID NO:3 for examination (see paper number 14). In response, Applicants wish to elect SEQ ID NO:61 for further examination. Claims 38-56 read on the all of the elected species.

The rejection of Claim 3 under 35 U.S.C. §102 over Pauley and Waterson is obviated in part by amendment and traversed in part.